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#29

RAW SEQUENCE LISTING

DATE: 04/17/2003

PATENT APPLICATION: US/09/732,436E

TIME: 10:43:43

Input Set : A:\Cura-115.app

Output Set: N:\CRF4\04172003\I732436E.raw

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3 <110> APPLICANT: Prayaga, Suhhirdas K
4   Shimkets, Richard A
6 <120> TITLE OF INVENTION: Novel Polypeptides and Polynucleotides Encoding Same
8 <130> FILE REFERENCE: 15966-615
10 <140> CURRENT APPLICATION NUMBER: 09/732,436E
11 <141> CURRENT FILING DATE: 2000-12-07
13 <150> PRIOR APPLICATION NUMBER: 60/169,887
14 <151> PRIOR FILING DATE: 1999-12-09
16 <150> PRIOR APPLICATION NUMBER: 60/170,230
17 <151> PRIOR FILING DATE: 1999-12-10
19 <160> NUMBER OF SEQ ID NOS: 27
21 <170> SOFTWARE: PatentIn Ver. 2.1
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25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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31 cagcctcttt ttacacaagg gcttgtctga tgcttgaat agggccttcc tggacaaact 180
32 ccagactgga tttcatcagc agctggaaga cctggagacc tgctttggta tagaggatgg 240
33 gaagcaagag tctgccttgg aaattgaggg ccctacactg gccataaaga ggtacttcca 300
34 gggagtacat ttcttcttga aagagaggaa attcaggaac tgtacctggg aggttgtcgt 360
35 aatggtaaaag ggatttttct taagcacaaa acttcaagaa aaagagaaca gaagaaaaga 420
36 gaactgcaaa aaaaatctgg aaaaggtaat ctatttagca gaagagtgaag agctg 475
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48 Ser Leu Phe Cys Asp Leu Pro Lys Ala Gln Val Ile Ser Ala Leu His
49 20 25 30
51 Lys Met His Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser
52 35 40 45
54 Asp Ala Trp Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His
55 50 55 60
57 Gln Gln Leu Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys
58 65 70 75 80
60 Gln Glu Ser Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg
61 85 90 95
63 Tyr Phe Gln Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn

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64          100          105          110
66 Cys Thr Trp Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr
67          115          120          125
69 Lys Leu Gln Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn
70          130          135          140
72 Leu Glu Lys Val Ile Tyr Leu Ala Glu Glu
73 145          150
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79 <213> ORGANISM: Homo sapiens
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83 <222> LOCATION: (74)..(208)
84 <223> OTHER INFORMATION: Wherein n is a or t or c or g.
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89 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 180
90 nnnnnnnnnn nnnnnnnnnn nnnnnnnnaa agctcaggtg atttctgccc tccataagat 240
91 gcaccagcag atcttcagcc tctttttaca caagggcttg tctgatgctt ggaatagggc 300
92 cttcctggac aaactccaga ctggatttca tcagcagctg gaagacctgg agacctgctt 360
93 tggatatagag gatgggaagc aagagtctgc cctggaaatt gagggcccta cactggccat 420
94 aaagaggtac ttccagggag tacatttctt cttgaaagag aggaaattca ggaactgtac 480
95 ctgggaggtt gtcgtaatgg taaagggatt tttcttaagc acaaaacttc aagaaaaaga 540
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97 gtgaaagctg                                     610
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103 <213> ORGANISM: Homo sapiens
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106 <221> NAME/KEY: VARIANT
107 <222> LOCATION: (24)..(68)
108 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
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112 1          5          10          15
W--> 114 Ser Leu Phe Cys Asp Leu Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa 20
115          20          25          30
117 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
118          35          40          45
120 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
121          50          55          60
123 Xaa Xaa Xaa Xaa Lys Ala Gln Val Ile Ser Ala Leu His Lys Met His
124 65          70          75          80
126 Gln Gln Ile Phe Ser Leu Phe Leu His Lys Gly Leu Ser Asp Ala Trp
127          85          90          95
129 Asn Arg Ala Phe Leu Asp Lys Leu Gln Thr Gly Phe His Gln Gln Leu

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130          100          105          110
132 Glu Asp Leu Glu Thr Cys Phe Gly Ile Glu Asp Gly Lys Gln Glu Ser
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135 Ala Leu Glu Ile Glu Gly Pro Thr Leu Ala Ile Lys Arg Tyr Phe Gln
136          130          135          140
138 Gly Val His Phe Phe Leu Lys Glu Arg Lys Phe Arg Asn Cys Thr Trp
139 145          150          155          160
141 Glu Val Val Val Met Val Lys Gly Phe Phe Leu Ser Thr Lys Leu Gln
142          165          170          175
144 Glu Lys Glu Asn Arg Arg Lys Glu Asn Cys Lys Lys Asn Leu Glu Lys
145          180          185          190
147 Val Ile Tyr Leu Ala Glu Glu
148          195
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152 <211> LENGTH: 1887
153 <212> TYPE: DNA
154 <213> ORGANISM: Homo sapiens
156 <400> SEQUENCE: 5
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158 cagtcagcca caccagccc atgtcccgc cgctgccgct gccagacaca gtcgctgcc 120
159 ctaagcgtgc tgtgccagg ggcaggcctc ctgttcgtgc caccctcgct ggaccgccg 180
160 gcagccgagc tgccggtggc agacaacttc atgcctccg tgcgccgcc cgacctggc 240
161 aacatgacag gcctgctgca tctgagcctg tcgcggaaca ccatccgcc cgtggctgcc 300
162 ggcgccctcg ccgacctgc ggccctgcgt gccctgcacc tggatggcaa ccggtgacc 360
163 tctactggcg agggccagct gcgcggcctg gtcaacttgc gccacctcat cctcagcaac 420
164 aaccagctgg cagcgtggc ggccggcgcc ctggatgatt gtgccgagac actggaggac 480
165 ctcgacctct cctacaacaa cctcgagcag ctgccctggg aggcctggg cgcctgggc 540
166 aacgtcaaca cgttgggcct cgaccacaac ctgctggctt ctgtgccgc cggcgcttt 600
167 tcccgccctg acaagctggc ccggtggac atgacctcca accgcctgac cacaatccca 660
168 cccgacccac tcttctcccg cctgcccctg ctgccaggc cccggggctc gccgcctct 720
169 gccctggtgc tggcctttgg cgggaacccc ctgcaactgc actgcgagct ggtgtggctg 780
170 cgtcgccctg cgccgggagga cgacctcgag gcctgcgcgt cccacctgc tctgggcggc 840
171 cgctacttct gggcggtggg cgaggaggag tttgtctgcg agccgccctg ggtgactcac 900
172 cgctcaccac ctctggtgtg gcccgaggt cgcccggtg ccctgcgctg ccgggcagt 960
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174 agccgtgccc gcgccttccc caatgggacg ctggagctgc tggtcaccga gccgggtgat 1080
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182 gaggacagcg ccacggggct cacggccacg cggcctgtgg gctgcgcccg cttctccacc 1560
183 gaacctgcgc tgcggccatg cggggcgccg cagctccct tcctgggcgg cacgatgatc 1620
184 atcgcgctgg gcggcgtcat cgtagcctcg gtactggtct tcatcttctg gctgctaata 1680
185 cgctacaagg tgcacggcgg ccagcccccc ggcaaggcca agattccgc gcctgttagc 1740
186 agcgtttgct cccagaccaa cggcgccctg ggccccacgc ccacgccgc cccgcccgcc 1800
187 ccggagcccc cggcgtcag ggcccacacc gtggtccagc tggactgcga gccctggggg 1860

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193 <212> TYPE: PRT
194 <213> ORGANISM: Homo sapiens
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201          20          25          30
203 Arg Cys Gln Thr Gln Ser Leu Pro Leu Ser Val Leu Cys Pro Gly Ala
204          35          40          45
206 Gly Leu Leu Phe Val Pro Pro Ser Leu Asp Arg Arg Ala Ala Glu Leu
207          50          55          60
209 Arg Leu Ala Asp Asn Phe Ile Ala Ser Val Arg Arg Arg Asp Leu Ala
210          65          70          75          80
212 Asn Met Thr Gly Leu Leu His Leu Ser Leu Ser Arg Asn Thr Ile Arg
213          85          90          95
215 His Val Ala Ala Gly Ala Phe Ala Asp Leu Arg Ala Leu Arg Ala Leu
216          100         105         110
218 His Leu Asp Gly Asn Arg Leu Thr Ser Leu Gly Glu Gly Gln Leu Arg
219          115         120         125
221 Gly Leu Val Asn Leu Arg His Leu Ile Leu Ser Asn Asn Gln Leu Ala
222          130         135         140
224 Ala Leu Ala Ala Gly Ala Leu Asp Asp Cys Ala Glu Thr Leu Glu Asp
225          145         150         155         160
227 Leu Asp Leu Ser Tyr Asn Asn Leu Glu Gln Leu Pro Trp Glu Ala Leu
228          165         170         175
230 Gly Arg Leu Gly Asn Val Asn Thr Leu Gly Leu Asp His Asn Leu Leu
231          180         185         190
233 Ala Ser Val Pro Ala Gly Ala Phe Ser Arg Leu His Lys Leu Ala Arg
234          195         200         205
236 Leu Asp Met Thr Ser Asn Arg Leu Thr Thr Ile Pro Pro Asp Pro Leu
237          210         215         220
239 Phe Ser Arg Leu Pro Leu Leu Ala Arg Pro Arg Gly Ser Pro Ala Ser
240          225         230         235         240
242 Ala Leu Val Leu Ala Phe Gly Gly Asn Pro Leu His Cys Asn Cys Glu
243          245         250         255
245 Leu Val Trp Leu Arg Arg Leu Ala Arg Glu Asp Asp Leu Glu Ala Cys
246          260         265         270
248 Ala Ser Pro Pro Ala Leu Gly Gly Arg Tyr Phe Trp Ala Val Gly Glu
249          275         280         285
251 Glu Glu Phe Val Cys Glu Pro Pro Val Val Thr His Arg Ser Pro Pro
252          290         295         300
254 Leu Ala Val Pro Ala Gly Arg Pro Ala Ala Leu Arg Cys Arg Ala Val
255          305         310         315         320
257 Gly Asp Pro Glu Pro Arg Val Arg Trp Val Ser Pro Gln Gly Arg Leu
258          325         330         335
260 Leu Gly Asn Ser Ser Arg Ala Arg Ala Phe Pro Asn Gly Thr Leu Glu

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261          340          345          350
263 Leu Leu Val Thr Glu Pro Gly Asp Gly Gly Ile Phe Thr Cys Ile Ala
264          355          360          365
266 Ala Asn Ala Ala Gly Glu Ala Thr Ala Ala Val Glu Leu Thr Val Gly
267          370          375          380
269 Pro Pro Pro Pro Pro Gln Leu Ala Asn Ser Thr Ser Cys Asp Pro Pro
270 385          390          395          400
272 Arg Asp Gly Asp Pro Asp Ala Leu Thr Pro Ser Ala Ala Ser Ala
273          405          410          415
275 Ser Ala Lys Val Ala Asp Thr Gly Pro Pro Thr Asp Arg Gly Val Gln
276          420          425          430
278 Val Thr Glu His Gly Ala Thr Ala Ala Leu Val Gln Trp Pro Asp Gln
279          435          440          445
281 Arg Pro Ile Pro Gly Ile Arg Met Tyr Gln Ile Gln Tyr Asn Ser Ser
282          450          455          460
284 Ala Asp Asp Ile Leu Val Tyr Arg Met Ile Pro Ala Glu Ser Arg Ser
285 465          470          475          480
287 Phe Leu Leu Thr Asp Leu Ala Ser Gly Arg Thr Tyr Asp Leu Cys Val
288          485          490          495
290 Leu Ala Val Tyr Glu Asp Ser Ala Thr Gly Leu Thr Ala Thr Arg Pro
291          500          505          510
293 Val Gly Cys Ala Arg Phe Ser Thr Glu Pro Ala Leu Arg Pro Cys Gly
294          515          520          525
296 Ala Pro His Ala Pro Phe Leu Gly Gly Thr Met Ile Ile Ala Leu Gly
297          530          535          540
299 Gly Val Ile Val Ala Ser Val Leu Val Phe Ile Phe Val Leu Leu Met
300 545          550          555          560
302 Arg Tyr Lys Val His Gly Gly Gln Pro Pro Gly Lys Ala Lys Ile Pro
303          565          570          575
305 Ala Pro Val Ser Ser Val Cys Ser Gln Thr Asn Gly Ala Leu Gly Pro
306          580          585          590
308 Thr Pro Thr Pro Ala Pro Pro Ala Pro Glu Pro Ala Ala Leu Arg Ala
309          595          600          605
311 His Thr Val Val Gln Leu Asp Cys Glu Pro Trp Gly Pro Gly His Glu
312          610          615          620
314 Pro Val Gly Pro
315 625
318 <210> SEQ ID NO: 7
319 <211> LENGTH: 802
320 <212> TYPE: DNA
321 <213> ORGANISM: Equus caballus
323 <400> SEQUENCE: 7
324 aaatcagaga tattataagt acacatatcc ctattaacgg cctagttggc aagaatgtca 60
325 tcagagaacc tcggtccaag ttcagagaca cccagctcag ccaggccagc agcaccctcg 120
326 ttttcccat ggccctcctg ccctctctct tgacggccct ggtggtgtac gagttatggc 180
327 cctgtggagc tctgggctgt gacctgcctc agaaccacat cctggttagc aggaagaact 240
328 tcgtgcttct gggccaaatg agcagaatct cctccgcaat ctgtctgaag gacagaaaag 300
329 acttcagggt cccccaggac atggcggatg gcaggcagtt cccagaggcc caggccgcgt 360
330 ctgtcctcca cgagatgctc cagcagatct tcagcctctt ccacacagag cgctcgtctg 420

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/732,436E

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TIME: 10:43:44

Input Set : A:\Cura-115.app
Output Set: N:\CRF4\04172003\I732436E.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93
Seq#:3; N Pos. 94,95,96,97,98,99,100,101,102,103,104,105,106,107,108,109
Seq#:3; N Pos. 110,111,112,113,114,115,116,117,118,119,120,121,122,123,124
Seq#:3; N Pos. 125,126,127,128,129,130,131,132,133,134,135,136,137,138,139
Seq#:3; N Pos. 140,141,142,143,144,145,146,147,148,149,150,151,152,153,154
Seq#:3; N Pos. 155,156,157,158,159,160,161,162,163,164,165,166,167,168,169
Seq#:3; N Pos. 170,171,172,173,174,175,176,177,178,179,180,181,182,183,184
Seq#:3; N Pos. 185,186,187,188,189,190,191,192,193,194,195,196,197,198,199
Seq#:3; N Pos. 200,201,202,203,204,205,206,207,208
Seq#:4; Xaa Pos. 24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42
Seq#:4; Xaa Pos. 43,44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61
Seq#:4; Xaa Pos. 62,63,64,65,66,67,68

VERIFICATION SUMMARY

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Input Set : A:\Cura-115.app

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L:88 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:60

M:341 Repeated in SeqNo=3

L:114 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:16

M:341 Repeated in SeqNo=4